THE EMBODIMENTS OF THE INVENTION IN WHICH AN EXCLUSIVE PROPERTY OF PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:

1. A method of regulating gene expression in a transgenic plant comprising, introducing into a plant:

i) a first chimeric nucleotide sequence comprising a first regulatory element in operative association with a gene of interest, and a controlling sequence; and

ii) a second chimeric nucleotide sequence comprising a second regulatory element in operative association with a nucleotide sequence encoding histone deaceytlase and a DNA binding protein, said DNA binding protein interacting with said controlling sequence, to produce said transgenic plant; and

iii) growing said transgenic plant.

2. The method of claim 1 wherein the step of introducing comprises sequentially transforming said plant with said first, and said second, chimeric nucleotide sequence, or co-transforming said plant with said first and said second chimeric nucleotide sequences.

3. The method of claim 1, wherein the step of introducing comprises transforming a first plant with said first chimeric nucleotide sequence, and transforming a second plant with said second chimeric nucleotide sequence, followed by a step of crossing said first and said second plant, to produce said transgenic plant.

4. The method of claim 1 wherein said histone deacetylase, within said step of introducing, is selected from the group consisting of *AtRPD3A*, *AtRPD3B*, *AtHD2A* *AtHD2B*, an analogue, fragment, or derivative of *AtRPD3A*, *AtRPD3B*, *AtHD2A* *AtHD2B*, and a nucleotide sequence that hybridizes to *AtRPD3A*, *AtRPD3B*, *AtHD2A* *AtHD2B* at 65°C in 0.5 M Na_2HPO_4 (pH 7.2), 7% SDS, and 1 mM EDTA, wherein said analog, fragment, derivative, or nucleotide sequence that hybridizes encodes a product that exhibits repression of gene expression activity.

5. The method of claim 1 wherein said first chimeric nucleotide sequence and the second chimeric nucleotide sequence, within said step of introducing, are contiguous within one construct.

6. The method of claim 1 wherein the first chimeric nucleotide sequence and the second chimeric nucleotide sequence, within said step of introducing, are separate constructs.

7. The method of claim 1 wherein said DNA binding protein, within the step of introducing, is selected from the group consisting of GAL4, AP2 domain proteins, APETALA2, PRbox binding protein, CCAAT-box binding proteins, LEC1 , BNM3, Pti4, and PICKLE.

8. The method of claim 1 wherein said first and said second regulatory region, within said step of introducing, are selected from the group consisting of constitutive, tissue specific, developmentally-regulated, and inducible regulatory elements.

9. An isolated nucleotide sequence, selected from the group consisting of:

i) SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7;

ii) an analog, derivative, fragment of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7; and

iii) a nucleotide sequence that hybridizes to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7 at 65°C in 0.5 M Na_2HPO_4 (pH 7.2), 7% SDS, and 1 mM EDTA,

wherein said analog, derivative, fragment or said nucleotide sequence that hybridizes encodes a product that exhibits repression of gene expression activity.

10. An isolated amino acid sequence, selected from the group consisting of:

i) SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8; and

ii) an analog, derivative, fragment of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8,

wherein said analog, derivative, or fragment exhibits repression of gene expression activity.

11. A chimeric construct comprising a regulatory element in operative association with said isolated nucleotide sequence of claim 9.

12. The chimeric construct of claim 11 further comprising a nucleotide sequence encoding a DNA binding protein.

13. A vector comprising said chimeric construct of claim 12.

14. A transgenic plant cell produced by the method of claim 1

15. A transgenic plant produced by the method of claim 1

16. A transgenic seed produced by the method of claim 1.

17. A transgenic plant comprising said isolated nucleotide sequence as defined by claim 9.

18. A transgenic plant cell comprising said isolated nucleotide sequence as defined by claim 9.

19. A transgenic seed comprising said isolated nucleotide sequence as defined by claim 9.

20.. A transgenic plant comprising said isolated amino acid sequence as defined in claim 10.

21. A method of regulating gene expression in a plant comprising,

i) introducing into the plant a chimeric nucleotide sequence comprising a regulatory element in operative association with a nucleotide sequence encoding histone deaceytlase and a nucleotide sequence encoding a DNA binding protein, to produce a transgenic plant; and

ii) growing said transgenic plant,

wherein said DNA binding protein has an affinity for a native controlling sequence within said plant.

22. The method of claim 21 wherein, said histone deacetylase, in the step of introducing, is defined in claim 9.

23. A method for identifying an endogenous DNA binding protein comprising:

i) introducing into an organism a chimeric nucleotide sequence comprising a nucleotide sequence encoding histone deaceytlase and a marker;

ii) growing said organism;

iii) screening mutants that exhibit a mutant phenotype and assaying for the presence of said marker to obtain a mutant organism; and

iv) isolating a nucleotide sequence comprising said endogenous DNA binding protein from said mutant organism.

24. The method of claim 23 wherein the step of introducing comprises a histone deacetylase as defined in claim 9.

25. A method for altering the development of an organism comprising:

i) introducing into an organism a chimeric nucleotide sequence comprising a regulatory element in operative association with a nucleotide sequence encoding histone deaceytlase and a nucleotide sequence encoding a DNA binding protein specific for a controlling sequence; and

ii) growing said organism.

26. The method of claim 25 wherein the step of introducing comprises a histone deacetylase as defined in claim 9.

27. A method for altering a biochemical, physiological or developmental pathway of an organism comprising:

i) introducing into an organism a chimeric nucleotide sequence comprising a regulatory element in operative association with a nucleotide sequence encoding histone deaceytlase and a nucleotide sequence encoding a DNA binding protein specific for a controlling sequence; and

ii) growing said organism.

28. A method for identifying a DNA binding protein comprising:

i) introducing into a plant a chimeric nucleotide sequence comprising a regulatory element in operative association with a nucleotide sequence encoding histone deaceytlase fused with a nucleotide sequence of interest and of unknown function, to produce a transgenic plant;

ii) growing said transgenic plant; and

iii) examining said transgenic plant to determine whether said chimeric nucleotide sequence, comprising said nucleotide sequence of interest has an effect on plant phenotype.